STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/553,906C
Source: EFW
Date Processed by STIC: 11/16/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED CORRECTION** **SERIAL NUMBER:** 10/553,906

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
3	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
4	Non-ASCII	The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
5	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence. <210> sequence id number <400> sequence id number 000
9	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
11	Use of <220>	Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13	Misuse of n/Xaa	"n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

IFWO

RAW SEQUENCE LISTING DATE: 11/16/2006
PATENT APPLICATION: **US/10/553,906C** TIME: 11:42:14

Input Set : **A:\PTO.SS.txt**
Output Set: **N:\CRF4\11162006\J553906C.raw**

This is NOT the invention title in the OFFICIAL U.S. Application. (See pg. 3)

Does Not Comply
Corrected Diskette Needed (pg. 1)

```
3 <110> APPLICANT: Skanemejerier AB
5 <120> TITLE OF INVENTION: NEW ENZYME AND ITS USE
7 <130> FILE REFERENCE: 75086
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/553,906C
C--> 9 <141> CURRENT FILING DATE: 2005-10-21
9 <150> PRIOR APPLICATION NUMBER: US 60/320,139
10 <151> PRIOR FILING DATE: 2003-04-24
12 <150> PRIOR APPLICATION NUMBER: US 60/481,598
13 <151> PRIOR FILING DATE: 2003-11-05
15 <160> NUMBER OF SEQ ID NOS: 18
17 <170> SOFTWARE: PatentIn version 3.2
```

See item 4 on error summary sheet.

ERRORED SEQUENCES

```
690 <210> SEQ ID NO: 18
691 <211> LENGTH: 31
692 <212> TYPE: DNA
693 <213> ORGANISM: Unknown
695 <220> FEATURE:
696 <223> OTHER INFORMATION: Artificial
698 <400> SEQUENCE: 18
699 acgtcgactt accagcacca taacagccaa g                    31
E--> 708 1
```

Same error in Seqs. 10-15, 17.

Invalid Response

Give source of genetic material.

(See item #11 on error Summary sheet.

1 pls delete

VERIFICATION SUMMARY DATE: 11/16/2006
PATENT APPLICATION: **US/10/553,906C** TIME: 11:42:16

Input Set : **A:\PTO.SS.txt**
Output Set: **N:\CRF4\11162006\J553906C.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:238 M:283 W: Missing Blank Line separator, <400> field identifier
L:401 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:900
L:708 M:254 E: No. of Bases conflict, this line has no nucleotides.

AMENDMENTS TO THE SPECIFICATION:

Applicant must Change 11207 response to this.

On page 1, before line 1, please insert:

-- Title of the Invention--

On page 1, please amend line 1 as follows:

~~NEW ENZYME AND ITS USE~~ Human Alkaline Sphingomyelinase and use thereof

On page 1, after line 1, please insert:

--Cross Reference to Related Applications

This application is a national stage application of International Application PCT/SE2004/000628, filed April 23, 2004, designating the United States of America, which claims the benefit of Provisional Patent Application No. 60/320,139, filed April 24, 2003 and Provisional Patent Application No. 60/481,598, filed November 5, 2003.

Field of the Invention--

Please replace the existing abstract with the following, which also follows on a separate sheet at the conclusion of this submission:

-- An isolated human alkaline sphingomyelinase (Alk-Smase) or a variant thereof is capable of hydrolysing sphingomyelin. Methods are provided for isolating human Alk-Smase and for preparing human recombinant Alk-Smase. Further methods are provided for the use of the enzyme for the treatment of colon cancer.--